From: Chan, Christina
Sent: Thursday, March 13, 2003 11:46 AM
T : Seharaseyon, Jegatheesan; STIC-Biotech/ChemLib
Subject: RE: RUSH Search Of 09/700590

Please rush. Thanks Chris

Chris Chan
TC 1600 New Hire Training Coordinator and SPE 1644′
308-3973
CM-1, 9B19

-----Original Message-----
From: Seharaseyon, Jegatheesan
Sent: Thursday, March 13, 2003 9:32 AM
To: Chan, Christina
Cc: O'Bryen, Barbara
Subject: RUSH Search Of 09/700590
Importance: High

Hi,
Please rush this search for me. Thanks.

1. Search the nucleotide encoding SEQ ID NO: 22 in the commerical database.
Also compare seq id no: 22 TO Acc. NO: CAA72780.1, AAC27978.1, CAA66186.1.

Thanks

J.Seharaseyon
Art Unit 1647
CM1 10D16
10B19 MB
Phone:(703)-305-1112
Fax: (703)-746-5177

Point of Contact:
Susan Hanley
Technical Info. Specialist
CM1 6B05 Tel: 305-4053

Searcher: _____	TYPE OF SEARCH:	VENDOR/COST (where applic.)
Searcher: _____	NA Sequences: _____	STN: _____
Phone: _____	AA Sequences: _____	DIALOG: _____
Location: _____	Structures: _____	Questel/Orbit: _____
Date Picked Up: _____	Bibliographic: _____	DRLink: _____
Date Completed: _____	Litigation: _____	Lexis/Nexis: _____
Searcher Prep/Review: _____	Full text: _____	Sequence Sys.: _____
Clerical: _____	Patent Family: _____	WWW/Internet: _____
Online time: _____	Other: _____	Other (specify): _____

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 22vspepl.res made by shanley on Mon 17 Mar 103 12:30:13-PST.

Query sequence being compared:US-09-700-590A-22 (1-688)
Number of sequences searched:        1
Number of scores above cutoff:       1

Results of the initial comparison of US-09-700-590A-22 (1-688) with:
        File : sehpep1.pep
```

```
    100-
         -
     50- -
         -
  N      -
  U      -
  M      -
  B      -
  E      -
  R      -
         -
  O   10-
  F      -
         -
  S    5-
  E      -
  Q      -
  U      -
  E      -
  N      -
  C      -                                                              *
  E      -
  S    0-|----|----|----|----|----|----|----|----|----|----|----|----|----|
            74  148  222  296  371  445  519  593  667
         SCORE 0
         STDEV
```

```
                    PARAMETERS
              Unitary         K-tuple                3
Similarity matrix  6          Joining penalty       30
Mismatch penalty  5.00        Window size          500
Gap penalty       0.33
Gap size penalty   0
Cutoff score       0
Randomization group

              SEARCH STATISTICS
Scores:        Mean      Median    Standard Deviation
               667        0          0.00

Times:          CPU                 Total Elapsed
         00:00:00.00               00:00:00.00

Number of residues:          731
Number of sequences searched:  1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                               Init.  Opt.
Sequence Name   Description                  Length Score Score Sig. Frame
--------------  -----------------------      ------ ----- ----- ---- -----
1. aac27978     TOIG of: aac27978  check: 531  731   667   667  0.00   0
```

```
1. US-09-700-590A-22 (1-688)
aac27978         TOIG of: aac27978  check: 5310  from: 1  to: 731

Initial Score    =   667   Optimized Score        =   667   Significance =  0.00
Residue Identity =    96%  Matches                =   667   Mismatches   =    21
Gaps             =     0   Conservative Substitutions =   0   Gaps       =     0
```

```
             10        20        30        40        50        60        70
       MSAESGPGTRLRNLPVMGDGLETSQMSTTQAQAQPQPANAASTNPPPPETSNPNKPKRQTNQLQYLLRVVLK
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
X      MSAESGPGTRLRNLPVMGDGLETSQMSTTQAQAQPQPANAASTNPPPPETSNPNKPKRQTNQLQYLLRVVLK
X      20        30        40        50        60        70        80

            80        90       100       110       120       130       140
       TLWKHQFAWPFQQPVDAVKLNLPDYYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGD
       ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       TLWKHQFAWPFQQPVDAVKLNLPDYYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGD
       90       100       110       120       130       140       150

           150       160       170       180       190       200       210
       DIVLMAEALEKLFLQKINELPTEETEIMIVQAKGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPP
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       DIVLMAEALEKLFLQKINELPTEETEIMIVQAKGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPP
       160       170       180       190       200       210       220

           220       230       240       250       260       270       280
       PVQATPHPFPAVTPDLIVQTPVMTVVPPQPLQTPPPVPPQPQPPAPAPQVQSHPPIIAATPQPVKTKKGV
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       PVQATPHPFPAVTPDLIVQTPVMTVVPPQPLQTPPPVPPQPQPPAPAPQVQSHPPIIAATPQPVKTKKGV
       230       240       250       260       270       280       290

           290       300       310       320       330       340       350       360
       KRKADTTTPTTIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKKDVPDSQQHPAPEKSSKVSEQLKCCSGI
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       KRKADTTTPTTIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKKDVPDSQQHPAPEKSSKVSEQLKCCSGI
       300       310       320       330       340       350       360       370

           370       380       390       400       410       420       430
       LKEMFAKKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKY
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       LKEMFAKKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKY
       380       390       400       410       420       430       440

           440       450       460       470       480       490       500
       NPPDHEVVAMARKLQDVFEMRFAKMPDEPEEPVVAVSSPAVPPPTKVVAPPSSSDSSSDSSSDSSTDDSE
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       NPPDHEVVAMARKLQDVFEMRFAKMPDEPEEPVVAVSSPAVPPPTKVVAPPSSSDSSSDSSSDSSTDDSE
       450       460       470       480       490       500       510

           510       520       530       540       550       560       570
       EERAQRLAELQEQLKAVHEQLAALSQPQQNKPKKKEKDKKEKHKEEVENKKSKAKEPPPKKTKKN
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       EERAQRLAELQEQLKAVHEQLAALSQPQQNKPKKKEKDKKEKHKEEVENKKSKAKEPPPKKTKKN
       520       530       540       550       560       570       580

           580       590       600       610       620       630       640
       NSSNSNVSKKEPAPMKSKPPPTYESEEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSN
       |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
       NSSNSNVSKKEPAPMKSKPPPTYESEEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSN
       590       600       610       620       630       640       650

           650       660       670       680         X
       PDEIEIDFETLKPSTLRELGALCHLLFAEEKETFKLRKLM
       ||||||||||||||||||||||||||||||||||||||||
       PDEIEIDFETLKPSTLRELGALCHLLFAEEKETFKLRKLM
       660       670       680       690         X
```

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 22vspep2.res made by shanley on Mon 17 Mar 103 12:31:25-PST.

Query sequence being compared:US-09-700-590A-22 (1-688)
Number of sequences searched:        1
Number of scores above cutoff:       1

Results of the initial comparison of US-09-700-590A-22 (1-688) with:
     File : sehpep2.pep
```

```
100-
    |
    |
N   |
U 50-
M   |
B   |
E   |
R   |
    |
O   |
F 10-
    |
S   |
E  5-
Q   |
U   |
E   |
N   |
C   |                                                        *
E   |
S  0------------------------------------------------------------
SCORE 0  8   16   23   31   39   47   54   62   70
STDEV    |    |    |    |    |    |    |    |    |
```

```
                    PARAMETERS

Similarity matrix    Unitary      K-tuple              3
Mismatch penalty        6         Joining penalty     30
Gap penalty          5.00         Window size        500
Gap size penalty     0.33
Cutoff score            0
Randomization group     0

                 SEARCH STATISTICS

Scores:          Mean    Median    Standard Deviation
                  70       0              0.00

Times:           CPU               Total Elapsed
             00:00:00.00           00:00:00.00

Number of residues:            128
Number of sequences searched:    1
Number of scores above cutoff:   1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```

```
                                                              Init.  Opt.
Sequence Name    Description                       Length Score Score  Sig.  Frame
---------------  ------------                       ------ ----- -----  ----  -----
 1. caa66186     TOIG of: caa66186  check: 205       128    70    70   0.00    0
```

```
 1. US-09-700-590A-22 (1-688)
    caa66186     TOIG of: caa66186  check: 2051  from: 1  to: 128

Initial Score      =   70    Optimized Score      =   70    Significance =  0.00
Residue Identity   =  75%    Matches              =   70    Mismatches   =  23
Gaps               =   0     Conservative Substitutions =  0              =   0
```

```
X 600      610       620       630       640       650       660
PPTYESEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSNPDEIEIDFETLKPSTLREL
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PPTYESEEDKCKPMSYEEKRHVSLDINKLPGEKLGRVVHIIQSREPSLKNSNPDEIEIDFETLKPSTLREL
X  10       20        30        40        50        60        70

670       680       X
GALCHLLFAEEKETFKLRKLM

ERYVTSCLRKKRKPQAEKVDV
  80        90       X
```

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OI IO   IntelliGenetics
> O <
FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 22vspep3.res made by shanley on Mon 17 Mar 103 12:32:45-PST.

Query sequence being compared:US-09-700-590A-22 (1-688)
File : sehpep3.pep
Number of sequences searched:      1
Number of scores above cutoff:     1
```

Results of the initial comparison of US-09-700-590A-22 (1-688) with:

```
Sequence Name      Description                           Length Score Score Sig. Frame
---------------    ---------------                       ------ ----- ----- ---- -----
                                                                      Init. Opt.
1.  ████caa72780██  TOIG of: caa72780  check: 720          722   667   667  0.00   0
```

1. US-09-700-590A-22 (1-688)
    caa72780   TOIG of: caa72780 check: 7201 from: 1 to: 722

```
Initial Score     =    667   Optimized Score        =    667   Significance   =   0.00
Residue Identity  =    96%   Matches                =    667   Mismatches     =    21
Gaps              =     0    Conservative Substitutions =  0   Gaps           =    0
```

```
         X        10        20        30        40        50        60        70
MSAESGPGTRLRNLPVMGDGLETSQMSTTQAQAQPQPANAASTNPPPPETSNPNKPKRQTNQLQYILLRVVLK
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
MSAESGPGTRLRNLPVMGDGLETSQMSTTQAQAQPQPANAASTNPPPPETSNPNKPKRQTNQLQYILLRVVLK
         X        10        20        30        40        50        60        70

        80        90       100       110       120       130       140
TLWKHQFAWPFQQPVDAVKLNLPDYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGD
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
TLWKHQFAWPFQQPVDAVKLNLPDYKIIKTPMDMGTIKKRLENNYYWNAQECIQDFNTMFTNCYIYNKPGD
        80        90       100       110       120       130       140

       150       160       170       180       190       200       210
DIVLMAEALEKLFLQKINELPTEETEIMIVQAKGRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPP
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
DIVLMAEALEKLFLQKINELPTEETEIMIVQAKGRGRGRKETGTAKPGVSTVPNTTQASTPPQTQTPQPNPP
       150       160       170       180       190       200       210

       220       230       240       250       260       270       280
PVQATPHPFPAVTPDLIVQTPVMTVVPPQPLQTPPPVPPQPQPPAPAPQPVQSHPPIIAATPQPVKTKKGV
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
PVQATPHPFPAVTPDLIVQTPVMTVVPPQPLQTPPPVPPQPQPPAPAPQPVQSHPPIIAATPQPVKTKKGV
       220       230       240       250       260       270       280

       290       300       310       320       330       340       350       360
KRKADTTTPTTIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKKDVPDSQQHPAPEKSSKVSEQLKCCSGI
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
KRKADTTTPTTIDPIHEPPSLPPEPKTTKLGQRRESSRPVKPPKKDVPDSQQHPAPEKSSKVSEQLKCCSGI
       290       300       310       320       330       340       350       360

       370       380       390       400       410       420       430
LKEMFAKKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKY
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
LKEMFAKKHAAYAWPFYKPVDVEALGLHDYCDIIKHPMDMSTIKSKLEAREYRDAQEFGADVRLMFSNCYKY
       370       380       390       400       410       420       430

       440       450       460       470       480       490       500
NPPDHEVVAMARKLQDVFEMRFAKMPDEPEPVVAVSSPAVPPPTKVVAPPSSSDSSSDSSSDSSSDSSTDDSE
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
NPPDHEVVAMARKLQDVFEMRFAKMPDEPEPVVAVSSPAVPPPTKVVAPPSSSDSSSDSSSDSSSDSSTDDSE
       440       450       460       470       480       490       500

       510       520       530       540       550       560       570
EERAQRLAELQEQLKAVHEQLAALSQPQQNKPKKKEKDKKEKKKEKHKRKEEVEENKKSKAKEPPKKTKKN
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
EERAQRLAELQEQLKAVHEQLAALSQPQQNKPKKKEKDKKEKKKEKHKRKEEVEENKKSKAKEPPKKTKKN
       510       520       530       540       550       560       570

       580       590       600       610       620       630       640
NSSNSNVSKKEPAPMKSKPPPTYSEEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSN
|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
NSSNSNVSKKEPAPMKSKPPPTYSEEEDKCKPMSYEEKRQLSLDINKLPGEKLGRVVHIIQSREPSLKNSN
       580       590       600       610       620       630       640

       650       660       670       680       X
PDEIEIDFETLKPSTLRELGALCHLLFAEEKETFKLRKLM
|||||||||||||||||||||||||
PDEIEIDFETLKPSTLRELERYVTSCLRKKRKPQAEKVDV
       650       660       670       680       X
```

```
                          100-
                     N      -
                     U    50-
                     M      -
                     B      -
                     E      -
                     R      -
                            -
                     O      -
                     F    10-
                            -
                     S     5-
                     E      -
                     Q      -
                     U      -
                     E      -                              *
                     N      -
                     C      -
                     E      -
                     S      0----|----|----|----|----|----|----|----|----|----|
                          SCORE 0   74  148  222  296  371  445  519  593  667
                          STDEV         0

                     PARAMETERS

          Similarity matrix    Unitary      K-tuple             3
          Mismatch penalty      6            Joining penalty    30
          Gap penalty           5.00         Window size        500
          Gap size penalty      0.33
          Cutoff score          0
          Randomization group   0

                     SEARCH STATISTICS

          Scores:        Mean      Median    Standard Deviation
                         667         0         0.00

          Times:        CPU                   Total Elapsed
                        00:00:00.00           00:00:00.00

          Number of residues:              722
          Number of sequences searched:      1
          Number of scores above cutoff:     1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:
```